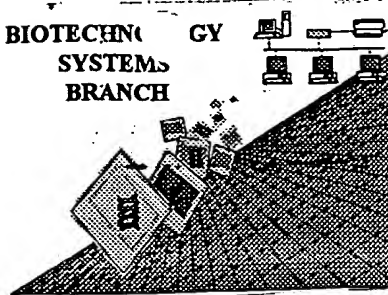
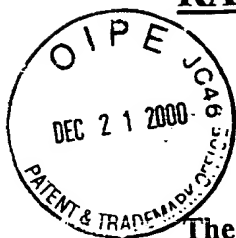


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0500

## **RAW SEQUENCE LISTING ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/728,421  
Source: OIPF  
Date Processed by STIC: 12/18/2000

OIPF/JCAG  
DEC 21 2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

#4

OIFE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
 TIME: 14:03:15

Does Not Comply  
 Corrected Diskette Needed

Input Set : A:\A-579-d.app  
 Output Set: N:\CRF3\12182000\I728421.raw

3 <110> APPLICANT: Yoshinaga, Steven K.  
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE  
 7 <130> FILE REFERENCE: A-579-D  
 OK> 9 <140> CURRENT APPLICATION NUMBER: US/09/728,421  
 10 <141> CURRENT FILING DATE: 2000-11-28  
 12 <160> NUMBER OF SEQ ID NOS: 35  
 14 <170> SOFTWARE: PatentIn Ver. 2.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 600  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: mouse  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 OK> 23 <222> LOCATION: Complement((1)..(600))  
 25 <400> SEQUENCE: 1  
 26 atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc ttc cta atc aga 48  
 27 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg  
 28 1 5 10 15  
 30 ctt tta aca gga gaa atc aat ggc tgc gcc gat cat agg atg ttt tca 96  
 31 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
 32 20 25 30  
 34 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144  
 35 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
 36 35 40 45  
 38 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192  
 39 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
 40 50 55 60  
 42 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240  
 43 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
 44 65 70 75 80  
 46 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288  
 47 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 48 85 90 95  
 50 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336  
 51 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
 52 100 105 110  
 54 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384  
 55 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
 56 115 120 125  
 58 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432  
 59 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 60 130 135 140  
 62 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480  
 63 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
 64 145 150 155 160  
 66 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528  
 67 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp

PR-4-5

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
 TIME: 14:03:15

Input Set : A:\A-579-d.app  
 Output Set: N:\CRF3\12182000\I728421.raw

```

68                               165               170               175
70 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576
71 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
72                               180               185               190
74 tct aga ctt gca ggt gtg acc tca 600
75 Ser Arg Leu Ala Gly Val Thr Ser
76                               195               200
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 200
81 <212> TYPE: PRT
82 <213> ORGANISM: mouse
84 <400> SEQUENCE: 2
85 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
86 1 5 10 15
88 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
89 20 25 30
91 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
92 35 40 45
94 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
95 50 55 60
97 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
98 65 70 75 80
100 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
101 85 90 95
103 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
104 100 105 110
106 Ile Phe Asp Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
107 115 120 125
109 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
110 130 135 140
112 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
113 145 150 155 160
115 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
116 165 170 175
118 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
119 180 185 190
121 Ser Arg Leu Ala Gly Val Thr Ser
122 195 200
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 200
128 <212> TYPE: PRT
129 <213> ORGANISM: mouse
131 <400> SEQUENCE: 3
132 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
133 1 5 10 15
135 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
136 20 25 30
138 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
139 35 40 45

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
 TIME: 14:03:15

Input Set : A:\A-579-d.app  
 Output Set: N:\CRF3\12182000\I728421.raw

```

141 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
142      50      55      60
144 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
145      65      70      75      80
147 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
148      85      90      95
150 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
151      100      105      110
153 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
154      115      120      125
156 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
157      130      135      140
159 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
160      145      150      155      160
162 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
163      165      170      175
165 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
166      180      185      190
168 Ser Arg Leu Ala Gly Val Thr Ser
169      195      200
172 <210> SEQ ID NO: 4
173 <211> LENGTH: 218
174 <212> TYPE: PRT
175 <213> ORGANISM: mouse
177 <400> SEQUENCE: 4
178 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
179      1      5      10      15
181 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
182      20      25      30
184 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
185      35      40      45
187 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
188      50      55      60
190 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
191      65      70      75      80
193 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
194      85      90      95
196 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
197      100      105      110
199 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
200      115      120      125
202 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
203      130      135      140
205 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
206      145      150      155      160
208 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
209      165      170      175
211 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
212      180      185      190

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
TIME: 14:03:15

Input Set : A:\A-579-d.app  
Output Set: N:\CRF3\12182000\I728421.raw

214 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala  
215 195 200 205  
217 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro  
218 210 215  
221 <210> SEQ ID NO: 5  
222 <211> LENGTH: 234  
223 <212> TYPE: PRT  
224 <213> ORGANISM: Artificial Sequence  
226 <220> FEATURE:  
227 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
228 Oglionucleotide  
230 <400> SEQUENCE:  
W--> 231 Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg  
232 1 10 15  
W--> 234 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
235 20 25 30  
W--> 237 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
238 35 40 45  
W--> 240 Val Xaa Xaa Ser Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
241 50 55 60  
W--> 243 Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa  
244 65 70 75 80  
W--> 246 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
247 85 90 95  
W--> 249 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Val Xaa Phe Xaa Leu  
250 100 105 110  
W--> 252 Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Cys Xaa Xaa Xaa  
253 115 120 125  
W--> 255 Xaa Xaa Xaa Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Gly Xaa  
256 130 135 140  
W--> 258 Xaa Xaa His Ile Xaa Glu Xaa Xaa Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa  
259 145 150 155 160  
W--> 261 Lys Leu Xaa Trp Xaa Leu Xaa Val Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa  
262 165 170 175  
W--> 264 Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Ile Trp Xaa Xaa Xaa  
265 180 185 190  
W--> 267 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa  
268 195 200 205  
W--> 270 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg  
271 210 215 220  
W--> 273 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
274 225 230  
277 <210> SEQ ID NO: 6  
278 <211> LENGTH: 966  
279 <212> TYPE: DNA  
280 <213> ORGANISM: mouse  
282 <220> FEATURE:  
283 <221> NAME/KEY: CDS  
W--> 284 <222> LOCATION: Complement((1)..(966))

→ This is an amino acid sequence. Give source of genetic material. See circled portion of item 12 on Envo Summary Sheet.

See item 10 on Envo Summary Sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
TIME: 14:03:15

Input Set : A:\A-579-d.app  
Output Set: N:\CRF3\12182000\I728421.raw

```

286 <400> SEQUENCE: 6
287 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct 48
288 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
289 1 5 10 15
291 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96
292 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
293 20 25 30
295 ctg ttc ttg ctg ctg ttg aqc agc ctc tgt gct gcc tct gca gag act 144
296 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
297 35 40 45
299 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac 192
300 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
301 50 55 60
303 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa 240
304 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
305 65 70 75 80
307 atc gaa aac cca gaa gtt tgc gtg act tac tac ctg cct tac aag tct 288
308 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
309 85 90 95
311 cca ggg atc aat gtg gac aqt tcc tac aag aac agg ggc cat ctg tcc 336
312 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
313 100 105 110
315 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc 384
316 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
317 115 120 125
319 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca 432
320 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
321 130 135 140
323 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg 480
324 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
325 145 150 155 160
327 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac 528
328 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
329 165 170 175
331 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca 576
332 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
333 180 185 190
335 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac 624
336 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
337 195 200 205
339 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat 672
340 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
341 210 215 220
343 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt 720
344 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
345 225 230 235 240
347 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att 768
348 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
349 245 250 255

```

**FYI:**

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
 PATENT APPLICATION: US/09/728,421

DATE: 12/18/2000  
 TIME: 14:03:16

Input Set : A:\A-579-d.app  
 Output Set: N:\CRF3\12182000\I728421.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:23 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((1)..(600))  
 L:231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:231 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
 L:234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 M:340 Repeated in SeqNo=5  
 L:237 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
 L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
 L:284 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: Complement((1)..(966))  
 L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
 L:589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
 L:589 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
 L:592 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
 L:592 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
 M:340 Repeated in SeqNo=10  
 L:595 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
 L:595 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
 L:598 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
 L:598 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
 L:601 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
 L:601 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10

VERIFICATION SUMMARY                      DATE: 12/18/2000  
PATENT APPLICATION: US/09/728,421        TIME: 14:03:16

Input Set : A:\A-579-d.app  
Output Set: N:\CRF3\12182000\I728421.raw

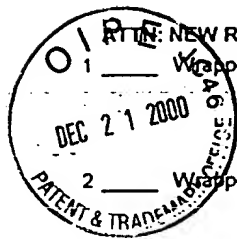
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:607 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:607 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:610 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:610 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:616 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:616 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:660 M:351 W: Sequence data Name/Key Feature Out-Of-Range, SEQ ID#:11, CDS LOCATION: Complement((1)..(864))  
L:927 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
M:340 Repeated in SeqNo=15  
L:1298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
M:340 Repeated in SeqNo=20



# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/728,421



NOTE: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length  
Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8        Skipped Sequences (OLD RULES)  
Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)  
Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)  
Sequence(s)        are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)  
Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.